```
CGCTATCCCTCCCTCGTACAAACAAACGCAAGAGCAGCAATGGCCGTCCAGAAGTACACG   60
                                       M  A  V  Q  K  Y  T
                                       -25            -20
GTGGCTCTATTCCTCGCCGTGGCCCTCGTGGCGGGCCCGGCCGCCTCCTACGCCGCTGAC  120
V  A  L  F  L  A  V  A  L  V  A  G  P  A  A  S  Y  A  A  D
         -15            -10            -5               1
GCCGGCTACACCCCCGCAGCCGCGGCCACCCCGGCTACTCCTGCTGCCACCCCGGCTGCG  180
A  G  Y  T  P  A  A  A  A  T  P  A  T  P  A  A  T  P  A  A
         5              10             15             20
GCTGGAGGGAAGGCGACGACCGACGAGCAGAAGCTGCTGGAGGACGTCAACGCTGGCTTC  240
A  G  G  K  A  T  T  D  E  Q  K  L  L  E  D  V  N  A  G  F
         25             30             35             40
AAGGCAGCCGTGGCCGCCGCTGCCAACGCCCCTCCGGCGGACAAGTTCAAGATCTTCGAG  300
K  A  A  V  A  A  A  A  N  A  P  P  A  D  K  F  K  I  F  E
         45             50             55             60
GCCGCCTTCTCCGAGTCCTCCAAGGGCCTCCTCGCCACCTCCGCCGCCAAGGCACCCGGC  360
A  A  F  S  E  S  S  K  G  L  L  A  T  S  A  A  K  A  P  G
         65             70             75             80
CTCATCCCCAAGCTCGACACCGCCTACGACGTCGCCTACAAGGCCGCCGAGGGCGCCACC  420
L  I  P  K  L  D  T  A  Y  D  V  A  Y  K  A  A  E  G  A  T
         85             90             95             100
CCCGAGGCCAAGTACGACGCCTTCGTCACTGCCCTCACCGAAGCGCTCCGCGTCATCGCC  480
P  E  A  K  Y  D  A  F  V  T  A  L  T  E  A  L  R  V  I  A
         105            110            115            120
GGCGCCCTCGAGGTCCACGCCGTCAAGCCCGCCACCGAGGAGGTCCCTGCTGCTAAGATC  540
G  A  L  E  V  H  A  V  K  P  A  T  E  E  V  P  A  A  K  I
         125            130            135            140
```

Fig. 1A

```
CCCACCGGTGAGCTGCAGATCGTTGACAAGATCGATGCTGCCTTCAAGATCGCAGCCACC   600
 P  T  G  E  L  Q  I  V  D  K  I  D  A  A  F  K  I  A  A  T
    145            150            155            160
GCCGCCAACGCCGCCCCCACCAACGATAAGTTCACCGTCTTCGAGAGTGCCTTCAACAAG   660
 A  A  N  A  A  P  T  N  D  K  F  T  V  F  E  S  A  F  N  K
    165            170            175            180
GCCCTCAATGAGTGCACGGGCGGCGCCTATGAGACCTACAAGTTCATCCCCTCCCTCGAG   720
 A  L  N  E  C  T  G  G  A  Y  E  T  Y  K  F  I  P  S  L  E
    185            190            195            200
GCCGCGGTCAAGCAGGCCTACGCCGCCACCGTCGCCGCCGCGCCCGAGGTCAAGTACGCC   780
 A  A  V  K  Q  A  Y  A  A  T  V  A  A  A  P  E  V  K  Y  A
    205            210            215            220
GTCTTTGAGGCCGCGCTGACCAAGGCCATCACCGCCATGACCCAGGCACAGAAGGCCGGC   840
 V  F  E  A  A  L  T  K  A  I  T  A  M  T  Q  A  Q  K  A  G
    225            230            235            240
AAACCCGCTGCCGCCGCTGCCACAGGCGCCGCAACCGTTGCCACCGGCGCCGCAACCGCC   900
 K  P  A  A  A  A  A  T  G  A  A  T  V  A  T  G  A  A  T  A
    245            250            255            260
GCCGCCGGTGCTGCCACCGCCGCTGCTGGTGGCTACAAAGCCTGATCAGCTTGCTAATAT   960
 A  A  G  A  A  T  A  A  A  G  G  Y  K  A  *
    265            270            275
ACTACTGAACGTATGTATGTGCATGATCCGGGCGGCGAGTGGTTTTGTTGATAATTAATC  1020
TTCGTTTTCGTTTCATGCAGCCGCGATCGAGAGGGCTTGCATGCTTGTAATAATTCAATA  1080
TTTTTCATTTCTTTTTGAATCTGTAAATCCCCATGACAAGTAGTGGGATCAAGTCGGCAT  1140
GTATCACCGTTGATGCGAGTTTAACGATGGGGAGTTTATCAAAGAATTTATTATTAAAAA  1200
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA                                 1229
```

Fig. 1B

LIX-1	ADAGYT<u>X</u>AAAAT<u>X</u>AT<u>X</u>AAT<u>X</u>
LIX-1.1	ADAGYTPAAAATPATPAATP
LIX-2	AT<u>X</u>AT<u>X</u>AAT<u>X</u>AAAGGKATTD
LIX-2.1	ATPATPAATPAAAGGKATTD
LIX-3	AAAGGKATTDEQKLLEDVNA
LIX-4	EQKLLEDVNAGFKAAVAAAA
LIX-5	GFKAAVAAAANAPPADKFKI
LIX-6	NAPPADKFKIFEAAFSESSK
LIX-7	FEAAFSESSKGLLATSAAKA
LIX-8	GLLATSAAKAPGLIPKLDTA
LIX-9	PGLIPKLDTAYDVAYKAAEG
LIX-10	YDVAYKAAEGATPEAKYDAF
LIX-11	ATPEAKYDAFVTALTEALRV
LIX-12	VTALTEALRVIAGALEVHAV
LIX-13	IAGALEVHAVKPATEEVPAA
LIX-14	KPATEEVPAAKIPTGELQIV
LIX-15	KIPTGELQIVDKIDAAFKIA
LIX-16	DKIDAAFKIAATAANAAPTN
LIX-17	ATAANAAPTNDKFTVFESAF
LIX-18	DKFTVFESAFNKALNECTGG
LIX-19	NKALNECTGGAYETYKFIPS
LIX-20	AYETYKFIPSLEAAVKQAYA
LIX-21	LEAAVKQAYAATVAAAPEVK
LIX-22	ATVAAAPEVKYAVFEAALTK
LIX-23	YAVFEAALTKAITAMTQAQK
LIX-24	AITAMTQAQKAGKPAAAAAT
LIX-25	AGKPAAAAATGAATVATGAA
LIX-26	GAATVATGAATAAAGAATAA
LIX-27	TAAAGAATAAAGGYKA

<u>X</u> REPRESENTS HYDROXYPROLINE RESIDUE

Fig. 2

PEPTIDE NAME	PEPTIDE SEQUENCE
LPI-1	IAKVPPGPNITAEYGDKWLD
LPI-1.1	IAKVXPGXNITAEYGDKWLD
LPI-2	TAEYGDKWLDAKSTWYGKPT
LPI-3	AKSTWYGKPTGAGPKDNGGA
LPI-4	GAGPKDNGGACGYKNVDKAP
LPI-4.1	GAGPKDNGGACGYKDVDKAP
LPI-5	CGYKDVDKAPFNGMTGCGNT
LPI-6	FNGMTGCGNTPIFKDGRGCG
LPI-7	PIFKDGRGCGSCFEIKCTKP
LPI-8	SCFEIKCTKPESCSGEAVTV
LPI-9	ESCSGEAVTVTITDDNEEPI
LPI-10	TITDDNEEPIAPYHFDLSGH
LPI-11	APYHFDLSGHAFGSMADDGE
LPI-11.1	APYHFDLSGHAFGSMAKKGE
LPI-12	AFGSMADDGEEQKLRSAGEL
LPI-12.1	AFGSMAKKGEEQKLRSAGEL
LPI-13	EQKLRSAGELELQFRRVKCK
LPI-14	ELQFRRVKCKYPDDTKPTFH
LPI-15	YPDDTKPTFHVEKASNPNYL
LPI-16	VEKASNPNYLAILVKYVDGD
LPI-16.1	VEKGSNPNYLAILVKYVDGD
LPI-17	AILVKYVDGDGDVVAVDIKE
LPI-18	GDVVAVDIKEKGKDKWIELK
LPI-19	KGKDKWIELKESWGAVWRID
LPI-20	ESWGAVWRIDTPDKLTGPFT
LPI-21	TPDKLTGPFTVRYTTEGGTK
LPI-22	VRYTTEGGTKSEVEDVIPEG
LPI-23	SEVEDVIPEGWKADTSYSAK

Fig. 3

App No.: 08/737904 Docket No.: IMI-040CP3
Inventor: Irwin J. Griffith, *et al.*
Title: T CELL EPITOPES OF RYEGRASS POLLEN ALLERGEN

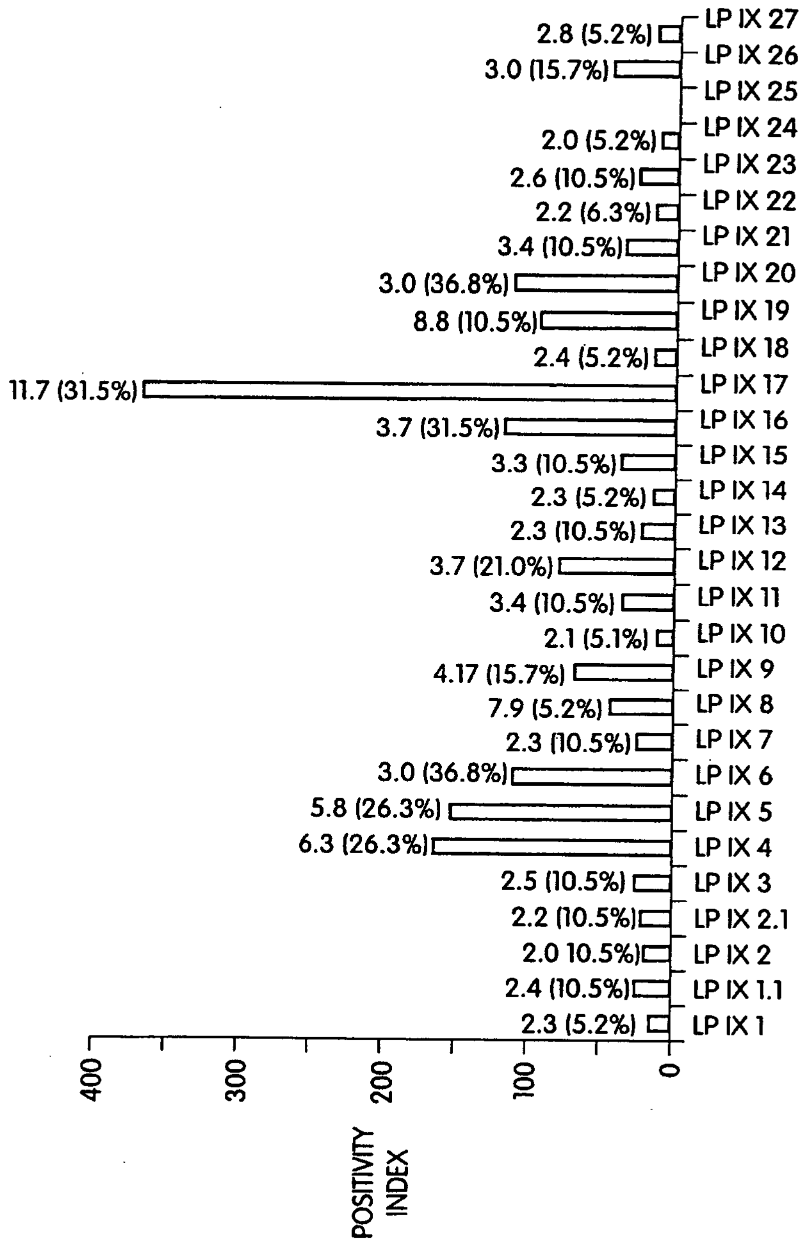

Fig. 4

App No.: 08/737904 Docket No.: IMI-040CP3
Inventor: Irwin J. Griffith, *et al.*
Title: T CELL EPITOPES OF RYEGRASS POLLEN ALLERGEN

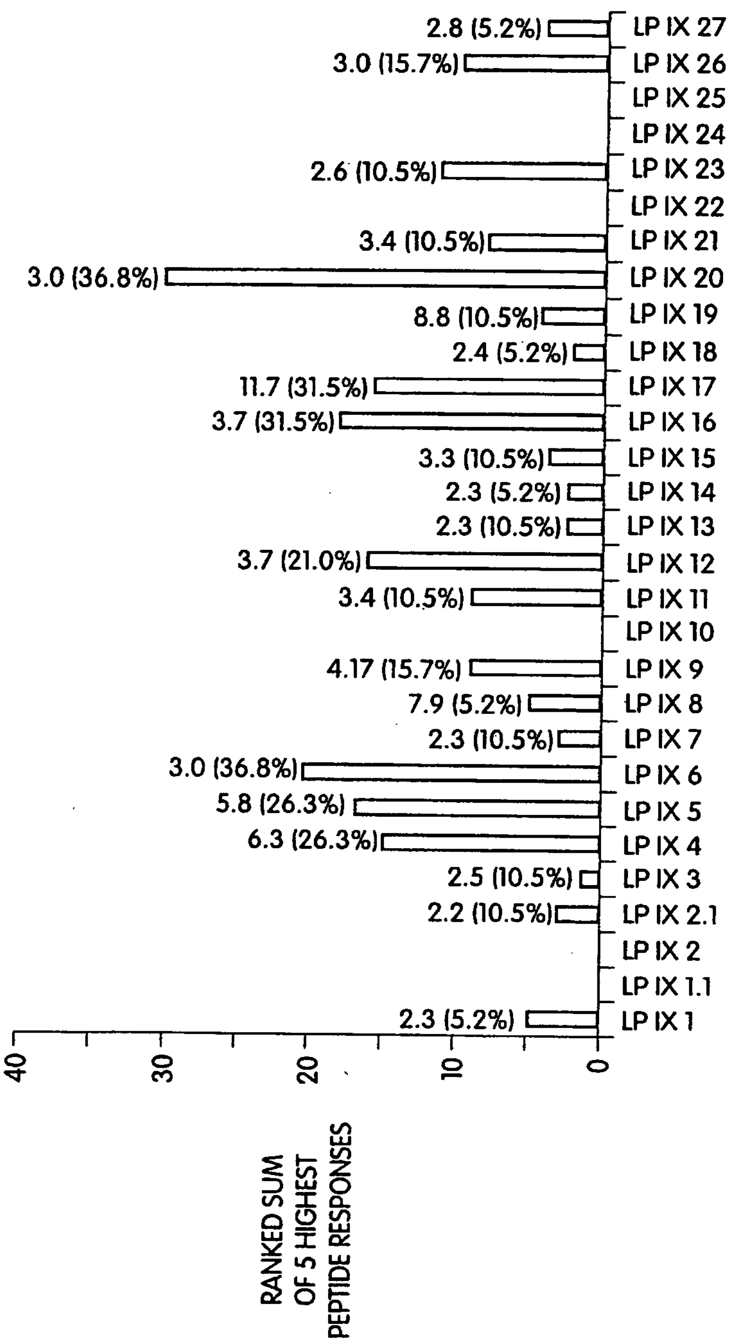

Fig. 5

App No.: 08/737904 Docket No.: IMI-040CP3
Inventor: Irwin J. Griffith, *et al.*
Title: T CELL EPITOPES OF RYEGRASS POLLEN ALLERGEN

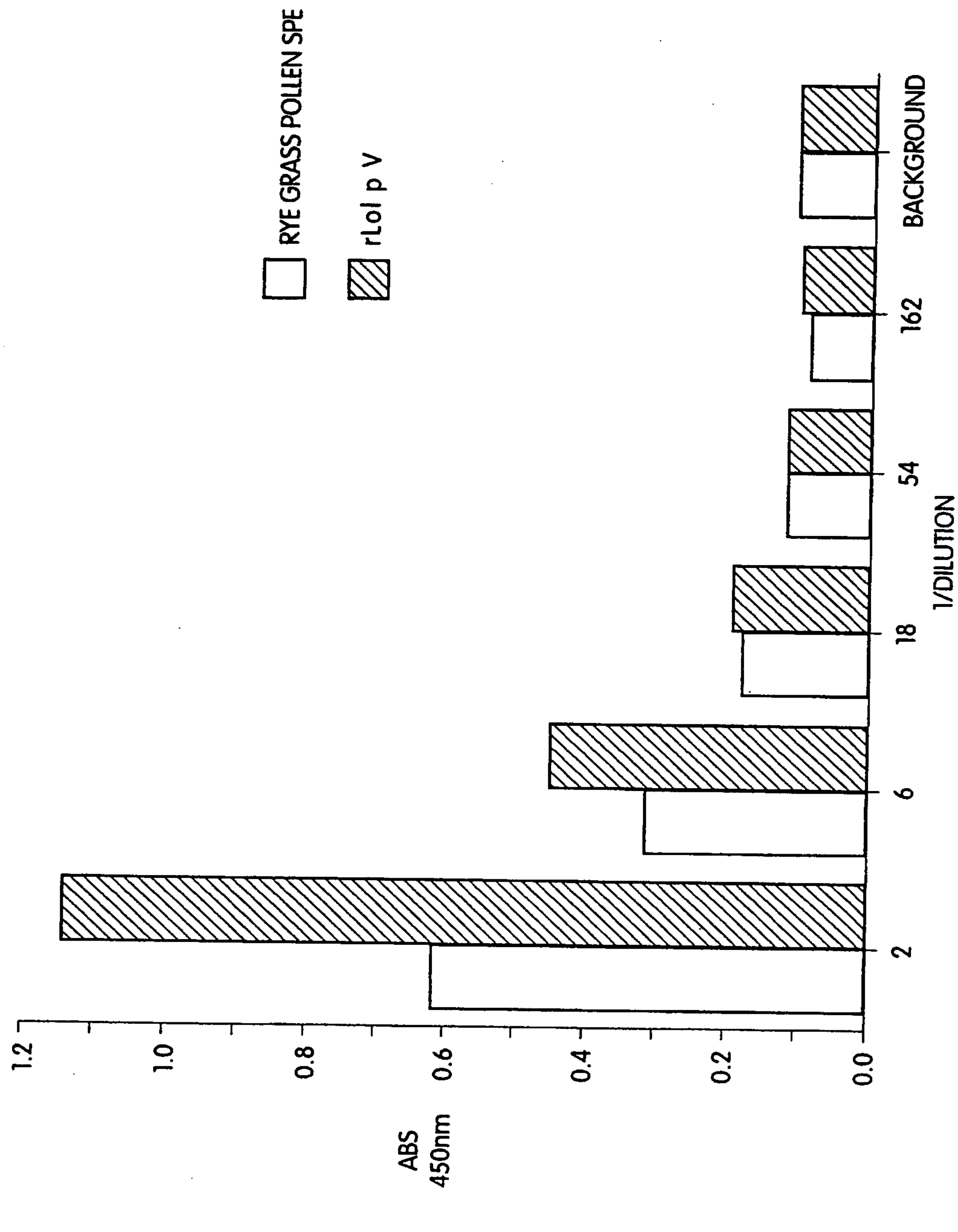

Fig. 6

App No.: 08/737904 Docket No.: IMI-040CP3
Inventor: Irwin J. Griffith, *et al.*
Title: T CELL EPITOPES OF RYEGRASS POLLEN ALLERGEN

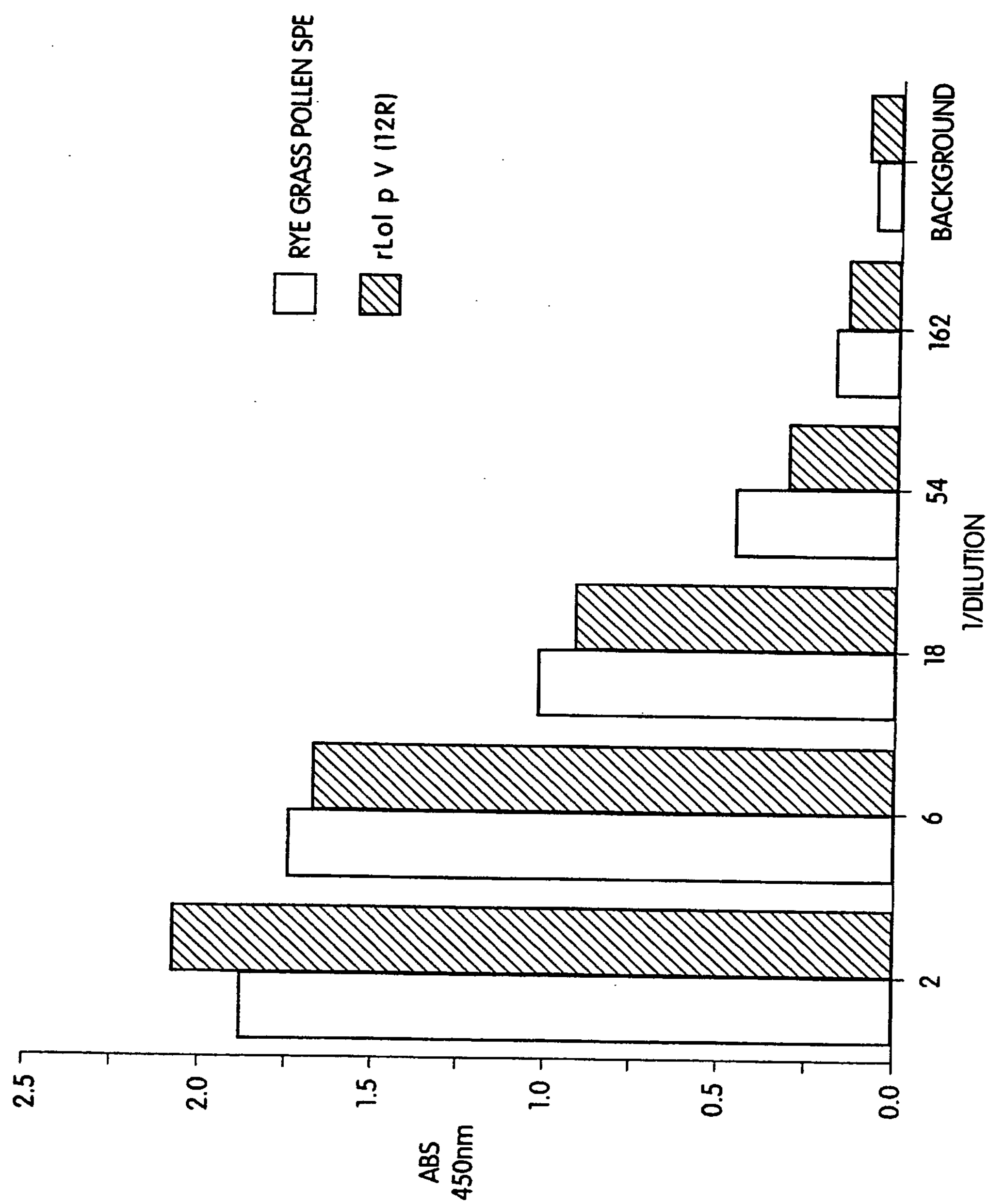

Fig. 7

App No.: 08/737904 Docket No.: IMI-040CP3
Inventor: Irwin J. Griffith, *et al.*
Title: T CELL EPITOPES OF RYEGRASS POLLEN ALLERGEN

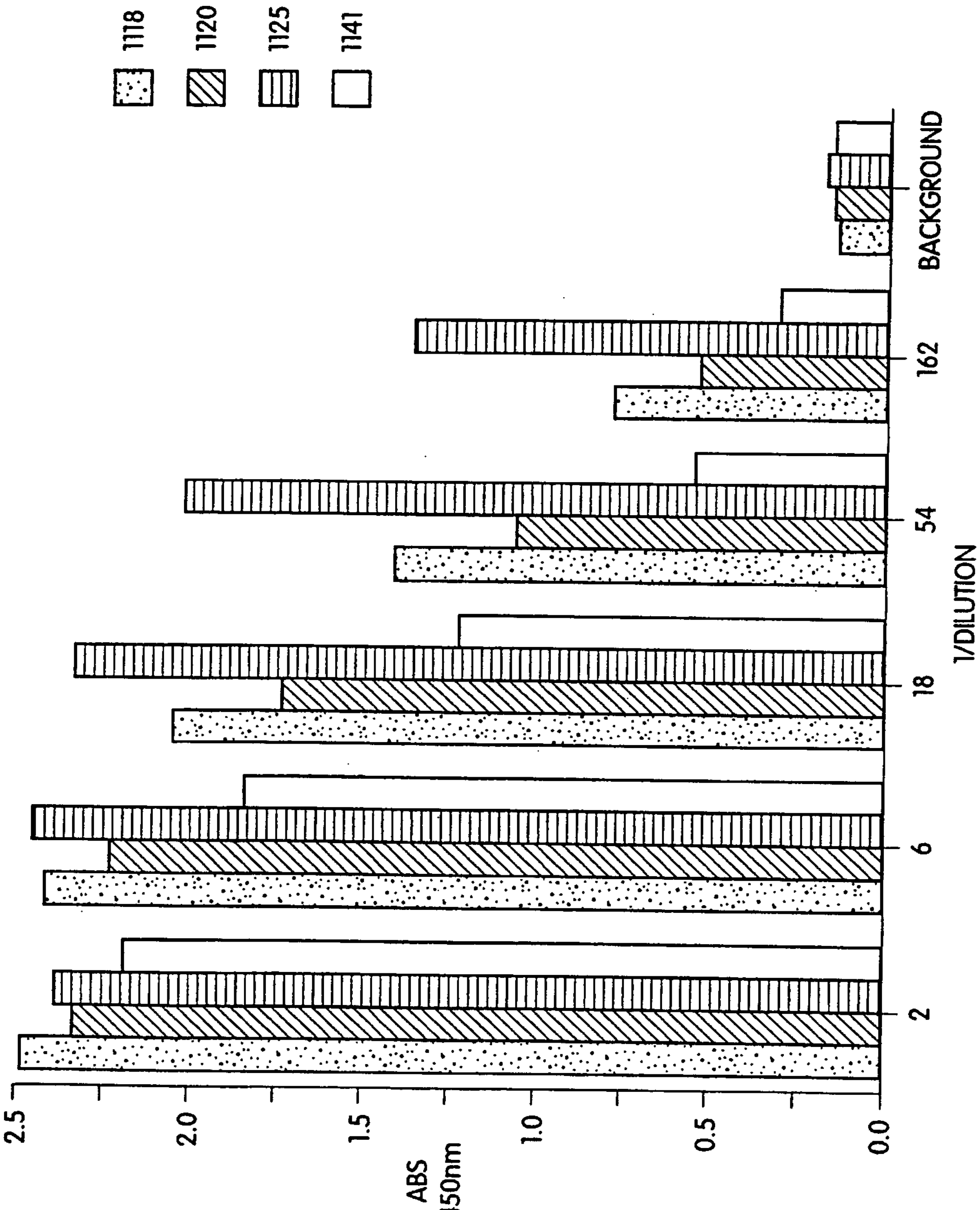

Fig. 8

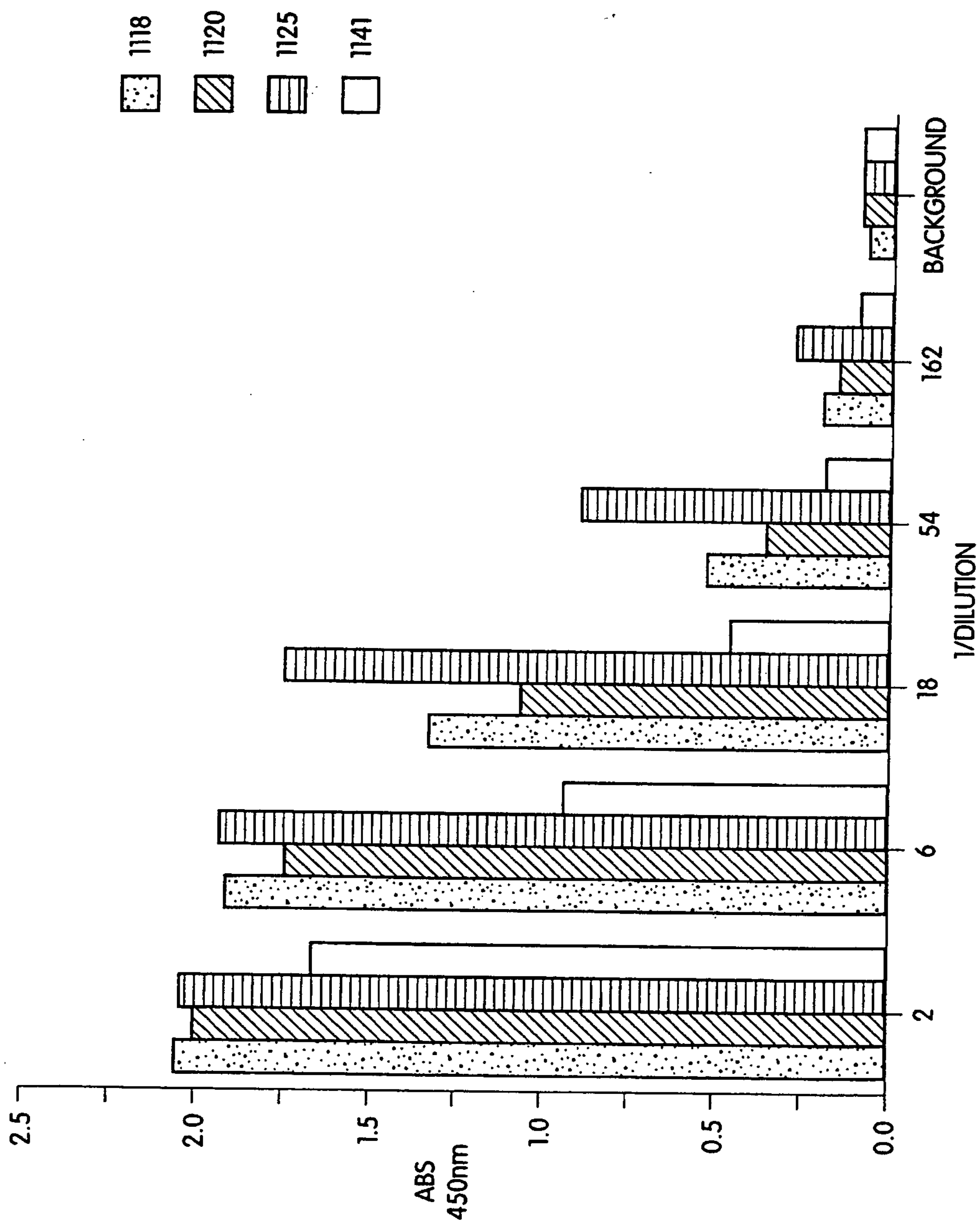
1118
1120
1125
1141
ABS
450nm
2.5
2.0
1.5
1.0
0.5
0.0
2
6
18
54
162
BACKGROUND
1/DILUTION

Fig. 9

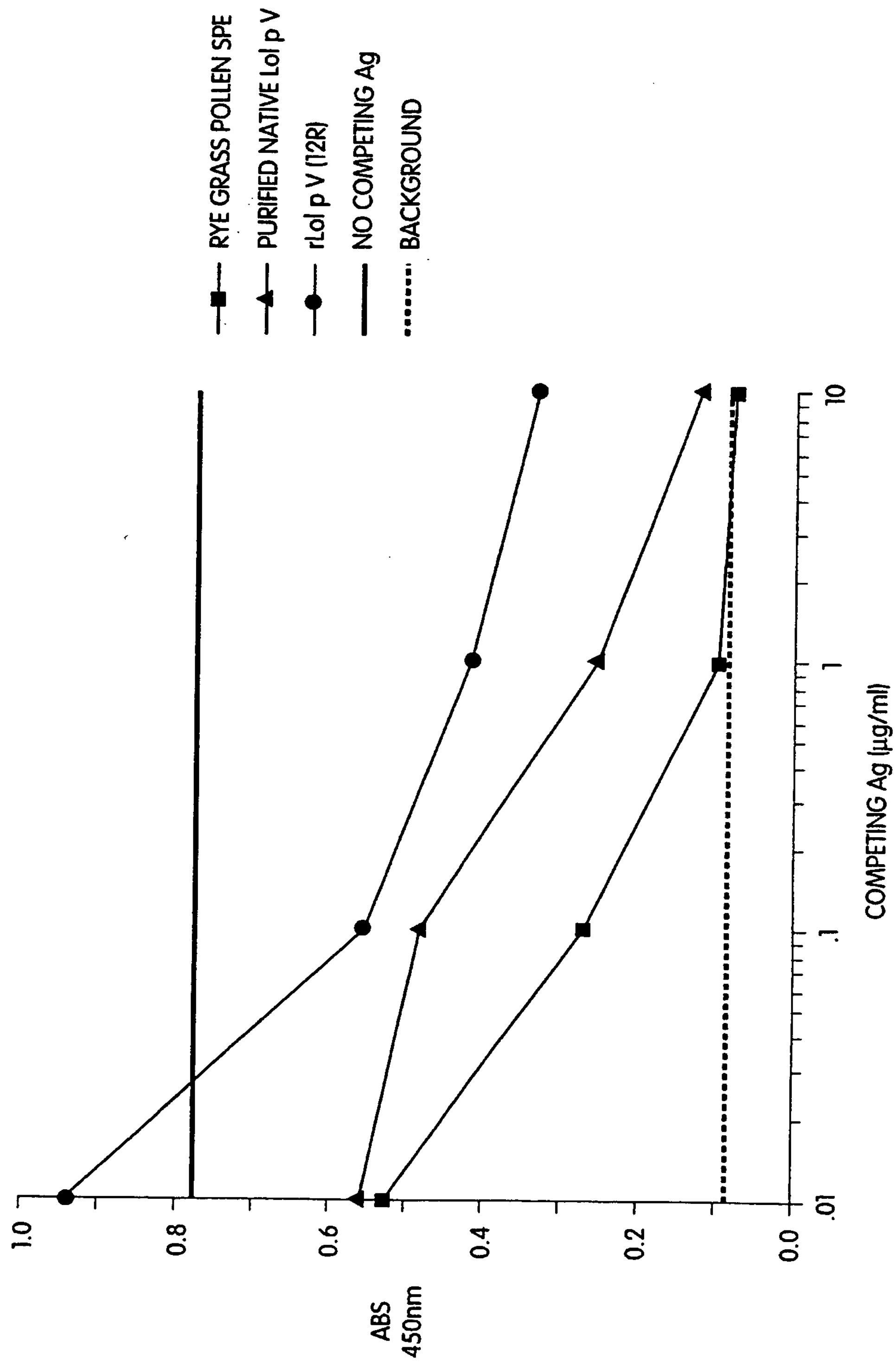
RYE GRASS POLLEN SPE
PURIFIED NATIVE Lol p V
rLol p V (12R)
NO COMPETING Ag
BACKGROUND
ABS 450nm
1.0
0.8
0.6
0.4
0.2
0.0
.01
.1
1
10
COMPETING Ag (µg/ml)

Fig. 10

App No.: 08/737904 Docket No.: IMI-040CP3
Inventor: Irwin J. Griffith, *et al.*
Title: T CELL EPITOPES OF RYEGRASS POLLEN ALLERGEN

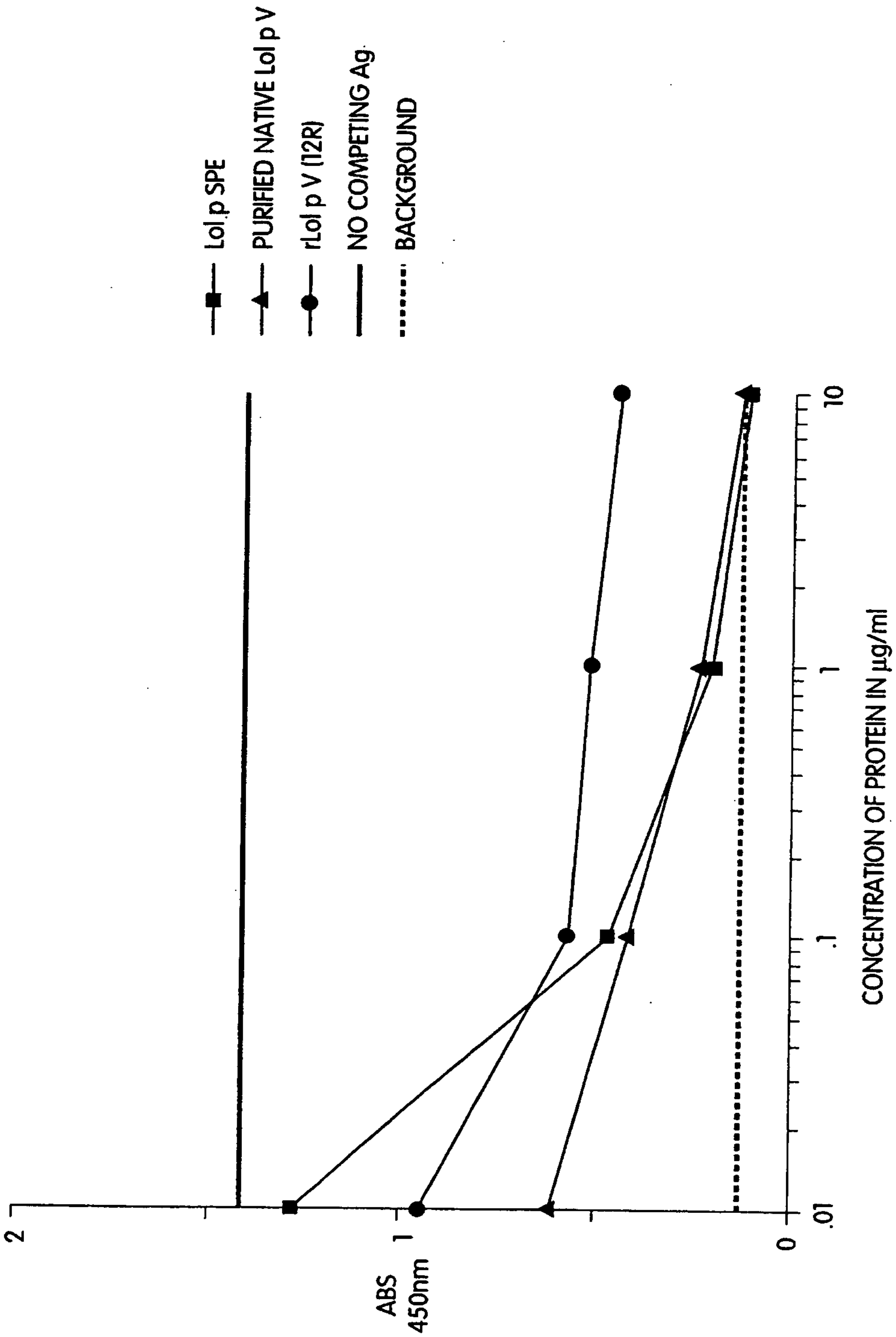

Fig. 11

App No.: 08/737904 Docket No.: IMI-040CP3
Inventor: Irwin J. Griffith, *et al.*
Title: T CELL EPITOPES OF RYEGRASS POLLEN ALLERGEN

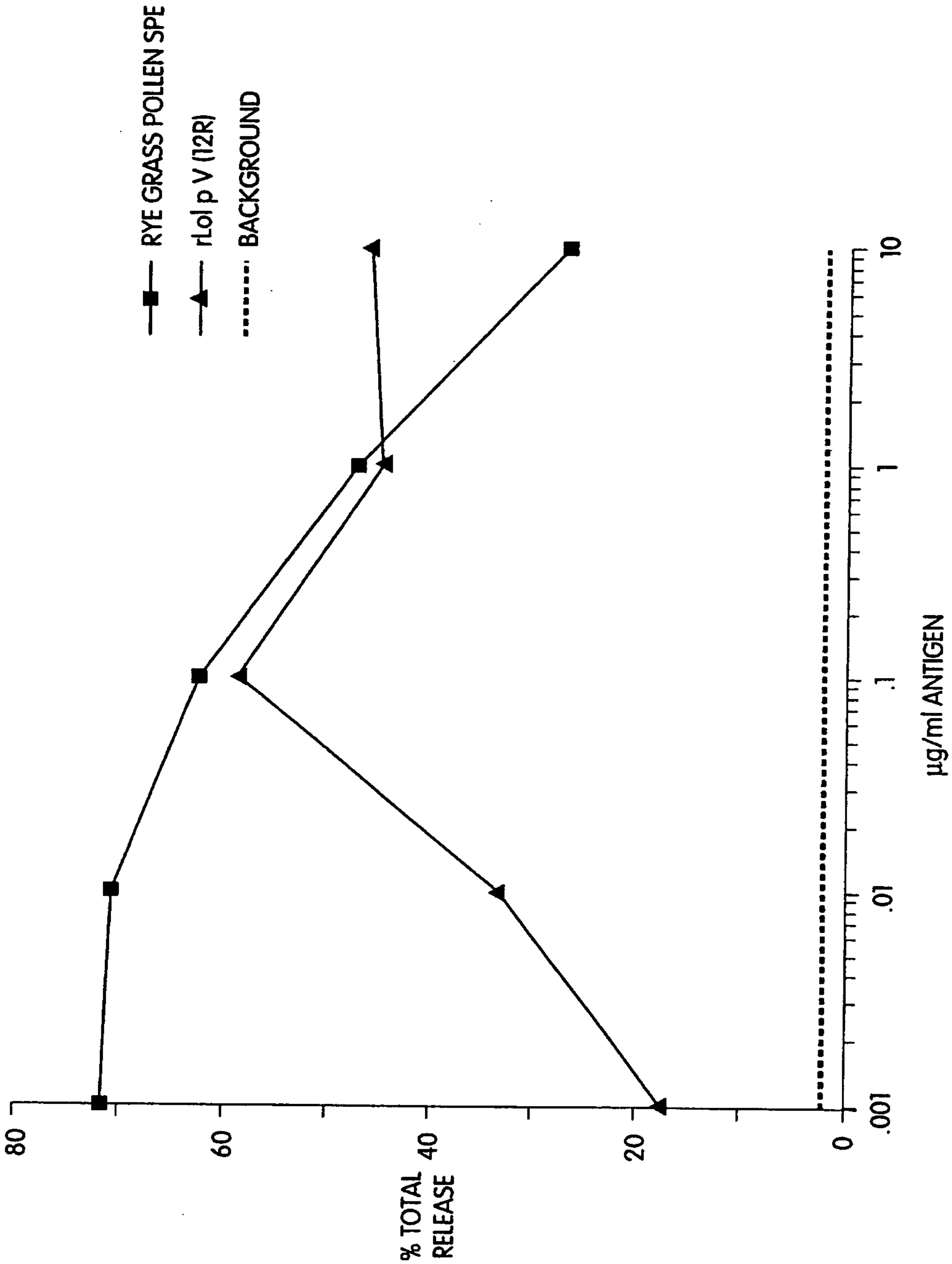

Fig. 12

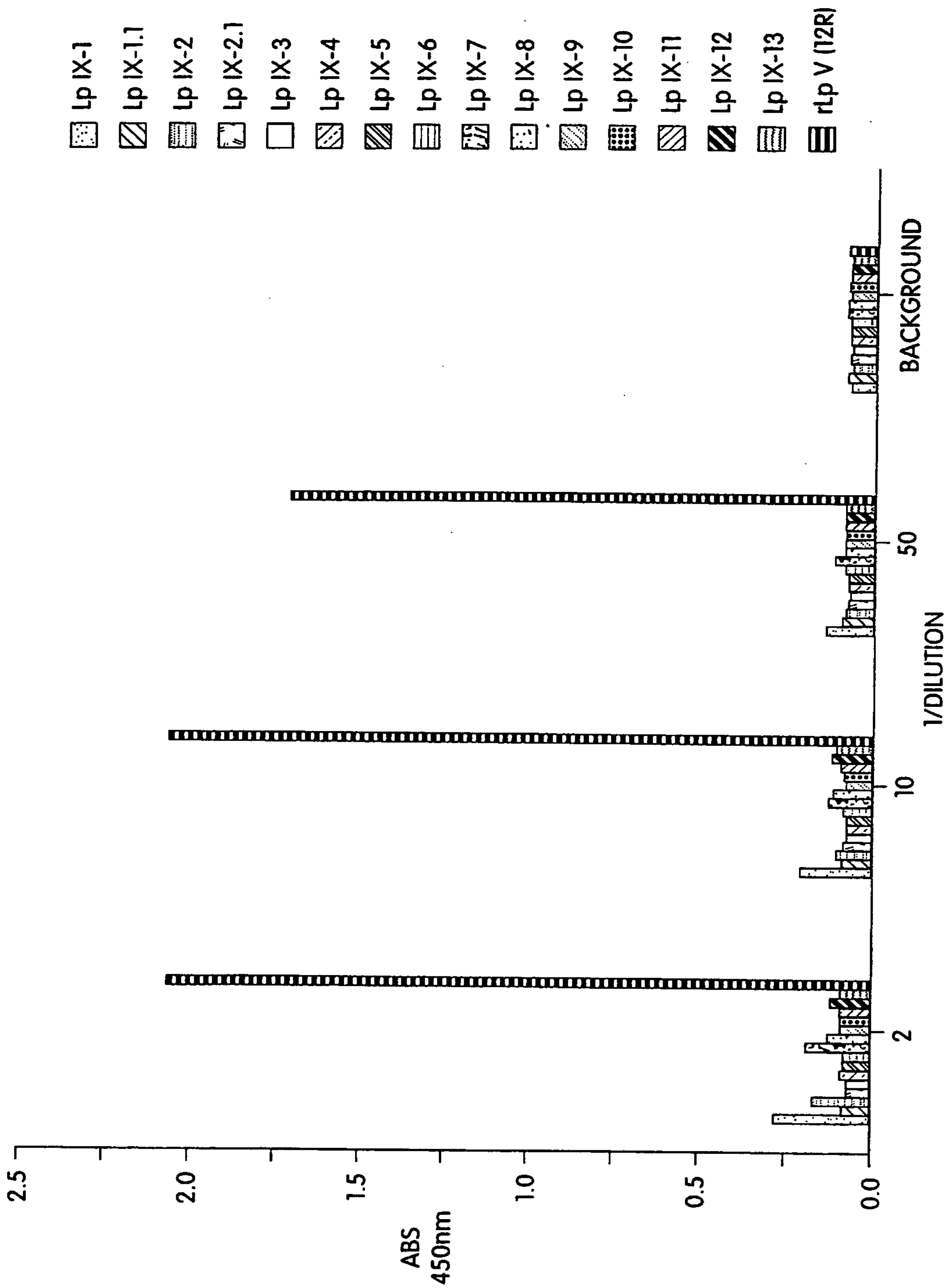
Lp IX-1
Lp IX-1.1
Lp IX-2
Lp IX-2.1
Lp IX-3
Lp IX-4
Lp IX-5
Lp IX-6
Lp IX-7
Lp IX-8
Lp IX-9
Lp IX-10
Lp IX-11
Lp IX-12
Lp IX-13
rLp V (12R)
ABS 450nm
2.5
2.0
1.5
1.0
0.5
0.0
2
10
50
BACKGROUND
1/DILUTION

Fig. 13A

App No.: 08/737904 Docket No.: IMI-040CP3
Inventor: Irwin J. Griffith, *et al.*
Title: T CELL EPITOPES OF RYEGRASS POLLEN ALLERGEN

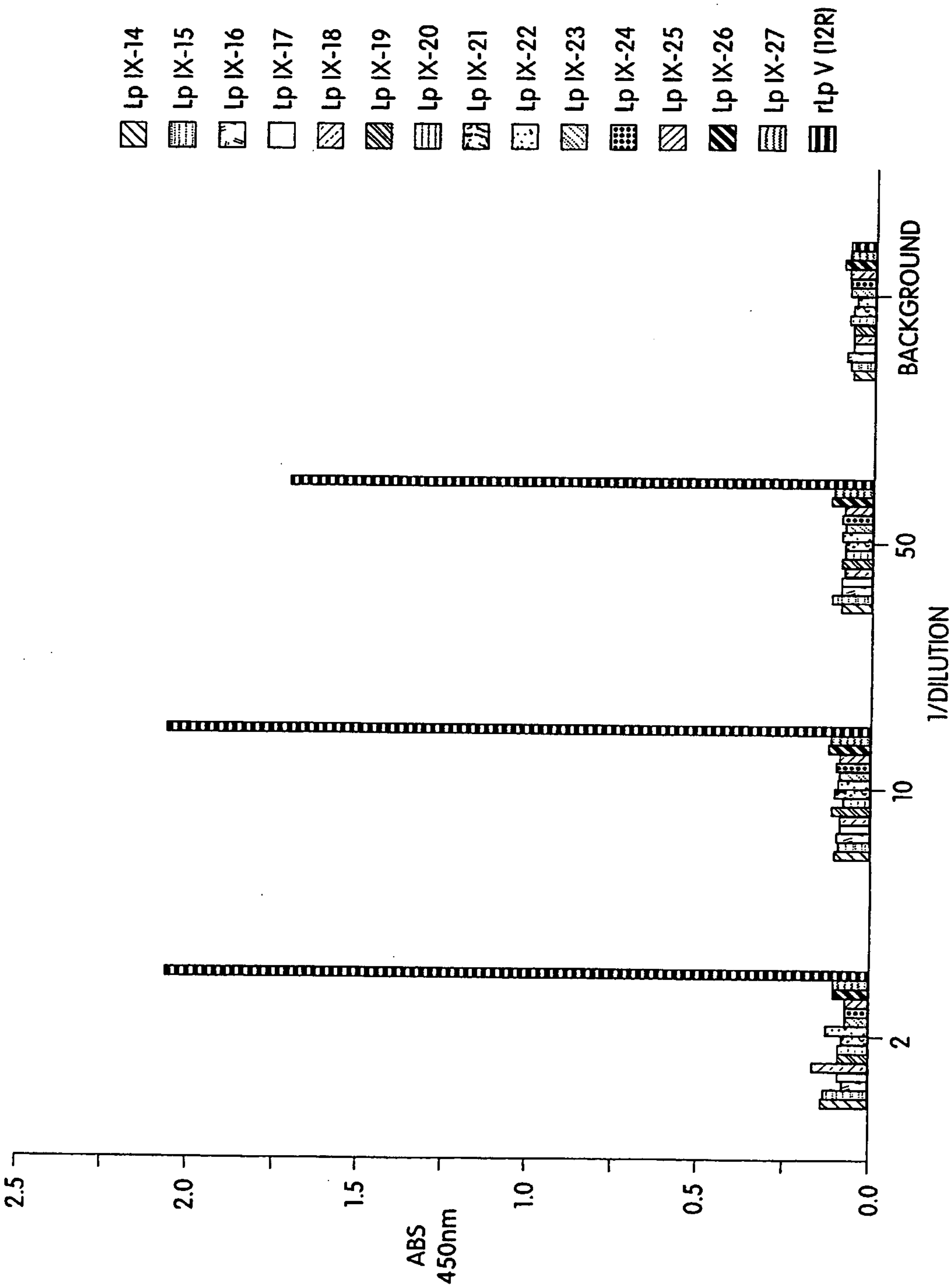

Fig. 13B

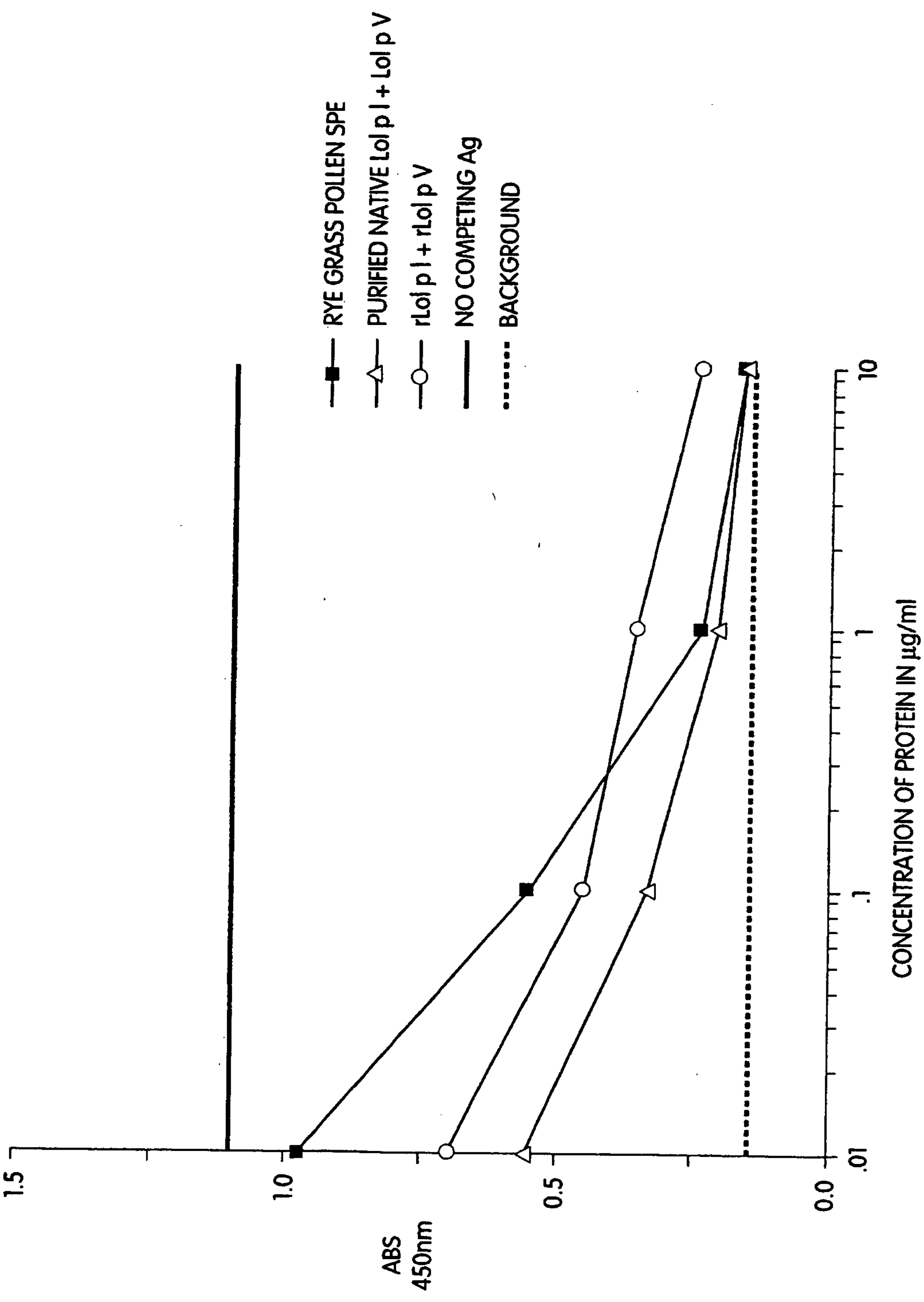
RYE GRASS POLLEN SPE
PURIFIED NATIVE Lol p I + Lol p V
rLol p I + rLol p V
NO COMPETING Ag
BACKGROUND
ABS
450nm
1.5
1.0
0.5
0.0
.01
.1
1
10
CONCENTRATION OF PROTEIN IN µg/ml

Fig. 14

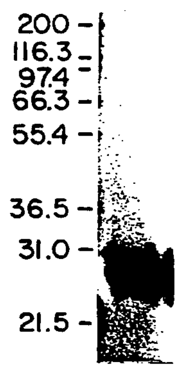

Fig. 15

```
GAATTCGAGGATCCGGGTACCATGGCTCCGACAAACCAACGCAAGAGCAGCAATGGCA    58
                                                      M  A
                                                    -24
GTGCAGCAGTACACGGTGGCGCTGTTCCTGGCCGTGGCCTCGTGTCGGGCCCGCGCCTCC  118
 V  Q  Q  Y  T  V  A  L  F  L  A  V  A  S  C  R  A  R  A  S
   -20                         -10
TACGCCGCCGACGCCGGCTACGCCCCCGCCACTCCCGCCACCCCGGCTACCCCCGCGGCC  178
 Y  A  A  D  A  G  Y  A  P  A  T  P  A  T  P  A  T  P  A  A
       1                       10
CCAGGCGCAGCGGTGCCAGCAGGGAAGGCGGCGACCGAGGAGCAGAAGCTGATCGAGAAG  238
 P  G  A  A  V  P  A  G  K  A  A  T  E  E  Q  K  L  I  E  K
   20                          30
ATCAACGCCGGCTTCAAGGCCGCCGTGGCGGCCGCCGCGGGCGTCCCGCCAGGCGACAAG  298
 I  N  A  G  F  K  A  A  V  A  A  A  A  G  V  P  P  A  D  K
   40                          50
TACAAGACGTTCGTCGAAACCTTCGGCAAGGCCTCCAACAAGGCCTTCCTGGGGGACCTC  358
 Y  K  T  F  V  E  T  F  G  K  A  S  N  K  A  F  L  G  D  L
   60                          70
CCGACCAACTACGCCGATGTCAACTCCAGGGCCCAGCTCACCTCGAAGCTCGACGCCGCC  418
 P  T  N  Y  A  D  V  N  S  R  A  Q  L  T  S  K  L  D  A  A
   80                          90
TACAAGCTCGCCTACGACGCCGCCCAGGGCGCCACCCCCGAGGCCAAGTACGACGCCTAC  478
 Y  K  L  A  Y  D  A  A  Q  G  A  T  P  E  A  K  Y  D  A  Y
  100                         110
```

Fig. 16A

```
GTCGCCACCCTCAGCGAGGCGCTCCGCATCATCGCCGGCACCCTCGAGGTCCACGCCGTC  538
 V  A  T  L  S  E  A  L  R  I  I  A  G  T  L  E  V  H  A  V
 120                           130
AAGCCCGCTGCCGAGGAGGTCAAGCCTATCCCCGCCGGAGAGCTGCAGATCGTCGACAAG  598
 K  P  A  A  E  E  V  K  P  I  P  A  G  E  L  Q  I  V  D  K
 140                           150
ATTGACGTCGCCTTCAGAACTGCCGCCACCGCCGCCAACGCCGCCCCCACCAACGACAAG  658
 I  D  V  A  F  R  T  A  A  T  A  A  N  A  A  P  T  N  D  K
 160                           170
TTCACCGTATTCGAGACCACCTTTAACAAGGCCATCAAGGAGAGCACGGGCGGCACCTAC  718
 F  T  V  F  E  T  T  F  N  K  A  I  K  E  S  T  G  G  T  Y
 180                           190
GAGAGCTACAAGTTCATTCCCACCCTTGAGGCCGCCGTTAAGCAGGCCTACGCCGCCACC  778
 E  S  Y  K  F  I  P  T  L  E  A  A  V  K  Q  A  Y  A  A  T
 200                           210
GTCGCATCCGCGCCGGAGGTCAAGTACGCCGTCTTTGAGACCGCGCTGAAAAAGGCGGTC  838
 V  A  S  A  P  E  V  K  Y  A  V  F  E  T  A  L  K  K  A  V
 220                           230
ACCGCCATGTCCGAGGCCCAGAAGGAAGCCAAGCCCGCCACCGCCACCCCGACCCCCACC  898
 T  A  M  S  E  A  Q  K  E  A  K  P  A  T  A  T  P  T  P  T
 240                           250
```

Fig. 16B

```
GCAACTGCCGCGGCCGCGGTGGCCACCAACGCCGCCCCCGTCGCTGCTGGTGGCTACAAA   958
 A  T  A  A  A  A  V  A  T  N  A  A  P  V  A  A  G  G  Y  K
  260                           270
ATCTGATCAACTCGCTAGCAATATACACATCCATCATGCACATATAGAGCTGTGTATGTA  1018
 I  *
TGTGCATGCATGCCGTGGCGCCGCGCAAGTTTGCTCATAATTAATTCTTGGTTTTCGTTG  1078
CTTGCATCCACGAGCGACCGAGCCCGTGGATAGTCGCATGTGTATGTAATTTTTTCTGAG  1138
AAATGTGTATATGTAATATATAATTGAGTACTAAAAAAAAAAA                   1181
```

Fig. 16C